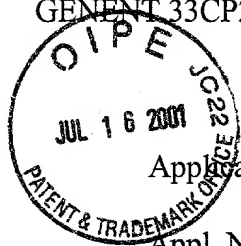


PATENT



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Presta et al.

) Group Art Unit: 1642

Appl. No. : 09/724,524

I hereby certify that this correspondence and all marked attachments are being deposited with the United States Postal Service as first-class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, D.C. 20231, on

Filed : November 27, 2000

For : HUMAN TRK RECEPTORS
AND NEUROTROPHIC
FACTOR INHIBITORS

July 11, 2001

(Date)

Ginger R. Dreger, Reg. No. 33,055

Examiner : Unknown

SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed on May 22, 2001.

I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a), included herewith, are supported in the application and that the Sequence Listing does not include new matter.

I hereby state that the computer readable form, submitted in accordance with 37 C.F.R. § 1.825(b), is the same as the paper form of the Sequence Listing.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: July 11, 2001

By: Wm. H.

Ginger R. Dreger

Registration No. 33,055

Attorney of Record

620 Newport Center Drive

Sixteenth Floor

Newport Beach, CA 92660

(415) 954-4114



Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.
Shelton, David L.
Urfer, Roman

(ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
(B) STREET: 620 Newport Center Drive 16th Floor
(C) CITY: Newport Beach
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: 09/724,524
(B) FILING DATE: 27-NOV-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/156,923
(B) FILING DATE: 18-SEP-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/359,705
(B) FILING DATE: 20-DEC-1994
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846
(B) FILING DATE: 10-AUG-1994

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139
(B) FILING DATE: 18-MAR-1994

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 949/760-0404

(B) TELEFAX: 949/760-9502

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3194 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
TTCGCCTGTC CCACGTCTTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
CGACCCTTCT CCTGGCATCG TGGCATTTC GAGATTGGAG CCTAACAGTG 300
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
CTCAGACCAC CACTGGTGCA TTCCATTCAC TGTGAAAGGC AACCCAAAAC 1050

CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
 CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
 CCTTTTGGA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500
 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600
 TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
 ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700
 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCGA 1750
 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800
 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950
 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000
 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCCAC 2050
 GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100
 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150
 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200
 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
 CAATGCTGCC CATTCGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300
 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400
 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450
 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500

GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550
CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650
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ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCAC CACAATAAC 3000
AATGCCTTGT TGTATTCTCG CCTTTGATGT GGATGAAAAA AAGGGAAAAAC 3050
AAATATTTCA CTTAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100
TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150
TTGGATGGCT TAAGCCTGTG TATAAAAAA AAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5					10					15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
			20						25					30
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys
			35						40					45
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro
			50						55					60
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn
			65						70					75
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr
			80						85					90
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe

				95					100					105
Val	Ala	His	Lys	Ala 110	Phe	Leu	Lys	Asn	Ser 115	Asn	Leu	Gln	His	Ile 120
Asn	Phe	Thr	Arg	Asn 125	Lys	Leu	Thr	Ser	Leu 130	Ser	Arg	Lys	His	Phe 135
Arg	His	Leu	Asp	Leu 140	Ser	Glu	Leu	Ile	Leu 145	Val	Gly	Asn	Pro	Phe 150
Thr	Cys	Ser	Cys	Asp 155	Ile	Met	Trp	Ile	Lys 160	Thr	Leu	Gln	Glu	Ala 165
Lys	Ser	Ser	Pro	Asp 170	Thr	Gln	Asp	Leu	Tyr 175	Cys	Leu	Asn	Glu	Ser 180
Ser	Lys	Asn	Ile	Pro 185	Leu	Ala	Asn	Leu	Gln 190	Ile	Pro	Asn	Cys	Gly 195
Leu	Pro	Ser	Ala	Asn 200	Leu	Ala	Ala	Pro	Asn 205	Leu	Thr	Val	Glu	Glu 210
Gly	Lys	Ser	Ile	Thr 215	Leu	Ser	Cys	Ser	Val 220	Ala	Gly	Asp	Pro	Val 225
Pro	Asn	Met	Tyr	Trp 230	Asp	Val	Gly	Asn	Leu 235	Val	Ser	Lys	His	Met 240
Asn	Glu	Thr	Ser	His 245	Thr	Gln	Gly	Ser	Leu 250	Arg	Ile	Thr	Asn	Ile 255
Ser	Ser	Asp	Asp	Ser 260	Gly	Lys	Gln	Ile	Ser 265	Cys	Val	Ala	Glu	Asn 270
Leu	Val	Gly	Glu	Asp 275	Gln	Asp	Ser	Val	Asn 280	Leu	Thr	Val	His	Phe 285
Ala	Pro	Thr	Ile	Thr 290	Phe	Leu	Glu	Ser	Pro 295	Thr	Ser	Asp	His	His 300
Trp	Cys	Ile	Pro	Phe 305	Thr	Val	Lys	Gly	Asn 310	Pro	Lys	Pro	Ala	Leu 315
Gln	Trp	Phe	Tyr	Asn 320	Gly	Ala	Ile	Leu	Asn 325	Glu	Ser	Lys	Tyr	Ile 330
Cys	Thr	Lys	Ile	His 335	Val	Thr	Asn	His	Thr 340	Glu	Tyr	His	Gly	Cys 345
Leu	Gln	Leu	Asp	Asn 350	Pro	Thr	His	Met	Asn 355	Asn	Gly	Asp	Tyr	Thr 360
Leu	Ile	Ala	Lys	Asn 365	Glu	Tyr	Gly	Lys	Asp 370	Glu	Lys	Gln	Ile	Ser 375
Ala	His	Phe	Met	Gly	Trp	Pro	Gly	Ile	Asp	Asp	Gly	Ala	Asn	Pro

380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn		
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr		
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala		
425	430	435
Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met		
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys		
455	460	465
Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro		
470	475	480
Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu		
485	490	495
Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val		
500	505	510
Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys		
515	520	525
Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu		
530	535	540
Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala		
545	550	555
Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala		
560	565	570
Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe		
575	580	585
His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile		
590	595	600
Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile Met		
605	610	615
Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg		
620	625	630
Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro		
635	640	645
Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile		
650	655	660
Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg		

GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTAAGT CCTGAATGAA 650
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050
CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500
GCATGAAAGG TTTTGTGTTG TTTTATAAGA TCCCACTGGA TGGGTAGCTG 1550
AAATAAGGA AAAGACAGAG AAAGGGGCTG TGGTGCTTGT TGGTTGATGC 1600
TGCCATGTAA GCTGGACTCC TGGGACTGCT GTTGGCTTAT CCCGGGAAGT 1650
GCTGCTTATC TGGGGTTTTT TGGTAGATGT GGGCGGTGTT TGGAGGCTGT 1700
ACTATATGAA GCCTGCATAT ACTGTGAGCT GTGATTGGGG AACACCAATG 1750
CAGAGGTAAC TCTCAGGCAG CTAAGCAGCA CCTCAAGAAA ACATGTTAAA 1800

TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAAC TG AAATGAAATC 1850

CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu	
1				5					10					15	
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe	
				20					25					30	
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	
				35					40					45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	
				50					55					60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	
				65					70					75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	
				80					85					90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	
				95					100					105	
Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	
				110					115					120	
Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	
				125					130					135	
Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe	
				140					145					150	
Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala	
				155					160					165	
Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser	
				170					175					180	
Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly	
				185					190					195	
Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu	
				200					205					210	
Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val	

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTG TAGTTT 50
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
CTCAGGACTT CGGAGCATTG AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800
TGTT CATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
GCTTACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
AGTGTTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950
GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000
CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
CCTGCTCTTC AACAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150
TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	
1				5					10					15	
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	
				20					25					30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	
				35					40					45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	
				50					55					60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	
				65					70					75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	
				80					85					90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	
				95					100					105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	
				110					115					120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	
				125					130					135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	
				140					145					150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	
				155					160					165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	
				170					175					180	
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	
				185					190					195	
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	
				200					205					210	
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	
				215					220					225	

Asn Ala Val Ile Thr Cys Asn Gly Ser	Gly Ser Pro Leu Pro Asp	230	235	240
Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln		245	250	255
Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu		260	265	270
Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile		275	280	285
Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr		290	295	300
Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu		305	310	315
Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro		320	325	330
Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser		335	340	345
Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu		350	355	360
Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn		365	370	375
Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr		380	385	390
Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp		395	400	405
Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr		410	415	420
Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala		425	430	435
Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe		440	445	450
Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys		455	460	465
Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro		470	475	480
Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp		485	490	495
Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val		500	505	510

Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	
				515					520					525	
Pro	Asp	Thr	Tyr	Val	Gln	His	Ile	Lys	Arg	Arg	Asp	Ile	Val	Leu	
				530					535					540	
Lys	Arg	Glu	Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	
				545					550					555	
Glu	Cys	Tyr	Asn	Leu	Ser	Pro	Thr	Lys	Asp	Lys	Met	Leu	Val	Ala	
				560					565					570	
Val	Lys	Ala	Leu	Lys	Asp	Pro	Thr	Leu	Ala	Ala	Arg	Lys	Asp	Phe	
				575					580					585	
Gln	Arg	Glu	Ala	Glu	Leu	Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	
				590					595					600	
Val	Lys	Phe	Tyr	Gly	Val	Cys	Gly	Asp	Gly	Asp	Pro	Leu	Ile	Met	
				605					610					615	
Val	Phe	Glu	Tyr	Met	Lys	His	Gly	Asp	Leu	Asn	Lys	Phe	Leu	Arg	
				620					625					630	
Ala	His	Gly	Pro	Asp	Ala	Met	Ile	Leu	Val	Asp	Gly	Gln	Pro	Arg	
				635					640					645	
Gln	Ala	Lys	Gly	Glu	Leu	Gly	Leu	Ser	Gln	Met	Leu	His	Ile	Ala	
				650					655					660	
Ser	Gln	Ile	Ala	Ser	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe	
				665					670					675	
Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Ala	Asn	
				680					685					690	
Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	
				695					700					705	
Ser	Thr	Asp	Tyr	Tyr	Arg	Leu	Phe	Asn	Pro	Ser	Gly	Asn	Asp	Phe	
				710					715					720	
Cys	Ile	Trp	Cys	Glu	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	
				725					730					735	
Trp	Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	
				740					745					750	
Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Ile	Phe	Thr	
				755					760					765	
Tyr	Gly	Lys	Gln	Pro	Trp	Phe	Gln	Leu	Ser	Asn	Thr	Glu	Val	Ile	
				770					775					780	
Glu	Cys	Ile	Thr	Gln	Gly	Arg	Val	Leu	Glu	Arg	Pro	Arg	Val	Cys	
				785					790					795	

Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu
800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His
815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly
830 835 839

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
CGGCGGCCCG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400
TGCGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800
TGTTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
GCTTCACCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
AGTGTGCCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950

GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000
 CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
 CCTGCTCTTC AACAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500
 GCCGGGCCCCG AACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
 GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAACTT GAAGGACAAT 1650
 AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700
 CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750
 TGTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800
 ATCTATGTTG AGGATGTCAA TGTTTATTTT AGCAAAGGAC GTCATGGCCT 1850
 TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 612 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5					10					15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu
			20						25					30
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
			35						40					45

Arg Arg Pro Asp Asp Gly Asn Leu Phe Pro Leu Leu Glu Gly Gln	50	55	60
Asp Ser Gly Asn Ser Asn Gly Asn Ala Asn Ile Asn Ile Thr Asp	65	70	75
Ile Ser Arg Asn Ile Thr Ser Ile His Ile Glu Asn Trp Arg Ser	80	85	90
Leu His Thr Leu Asn Ala Val Asp Met Glu Leu Tyr Thr Gly Leu	95	100	105
Gln Lys Leu Thr Ile Lys Asn Ser Gly Leu Arg Ser Ile Gln Pro	110	115	120
Arg Ala Phe Ala Lys Asn Pro His Leu Arg Tyr Ile Asn Leu Ser	125	130	135
Ser Asn Arg Leu Thr Thr Leu Ser Trp Gln Leu Phe Gln Thr Leu	140	145	150
Ser Leu Arg Glu Leu Gln Leu Glu Gln Asn Phe Phe Asn Cys Ser	155	160	165
Cys Asp Ile Arg Trp Met Gln Leu Trp Gln Glu Gln Gly Glu Ala	170	175	180
Lys Leu Asn Ser Gln Asn Leu Tyr Cys Ile Asn Ala Asp Gly Ser	185	190	195
Gln Leu Pro Leu Phe Arg Met Asn Ile Ser Gln Cys Asp Leu Pro	200	205	210
Glu Ile Ser Val Ser His Val Asn Leu Thr Val Arg Glu Gly Asp	215	220	225
Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp	230	235	240
Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln	245	250	255
Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu	260	265	270
Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile	275	280	285
Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr	290	295	300
Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu	305	310	315
Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro	320	325	330

Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	
				335					340					345	
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	
				350					355					360	
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	
				365					370					375	
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr	
				380					385					390	
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp	
				395					400					405	
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr	
				410					415					420	
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala	
				425					430					435	
Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe	
				440					445					450	
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys	
				455					460					465	
Gly	Pro	Val	Ala	Val	Ile	Ser	Gly	Glu	Glu	Asp	Ser	Ala	Ser	Pro	
				470					475					480	
Leu	His	His	Ile	Asn	His	Gly	Ile	Thr	Thr	Pro	Ser	Ser	Leu	Asp	
				485					490					495	
Ala	Gly	Pro	Asp	Thr	Val	Val	Ile	Gly	Met	Thr	Arg	Ile	Pro	Val	
				500					505					510	
Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	
				515					520					525	
Pro	Asp	Thr	Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	
				530					535					540	
Asn	Leu	Lys	Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	
				545					550					555	
Ile	Tyr	Glu	Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	
				560					565					570	
Arg	Ser	His	Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	
				575					580					585	
Pro	Gly	His	Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	
				590					595					600	
Val	Asn	Val	Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe				
				605					610		612				

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp	1	5	10	15
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser	20	25	30	
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser	35	40	45	
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His	50	55	60	
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn	65	70	75	
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu	80	85	90	
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe	95	100	105	
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu	110	115	120	
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val	125	130	135	
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu	140	145	150	
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	Glu	155	160	165	
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln	170	175	180	
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr	185	190	195	
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp	200	205	210	
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala	215	220	225	
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys	230	235	240	

Ser Gly Gly Leu Pro Ser Leu Gly Leu Thr Leu Ala Asn Val Thr	245	250	255
Ser Asp Leu Asn Arg Lys Asn Leu Thr Cys Trp Ala Glu Asn Asp	260	265	270
Val Gly Arg Ala Glu Val Ser Val Gln Val Asn Val Ser Phe Pro	275	280	285
Ala Ser Val Gln Leu His Thr Ala Val Glu Met His His Trp Cys	290	295	300
Ile Pro Phe Ser Val Asp Gly Gln Pro Ala Pro Ser Leu Arg Trp	305	310	315
Leu Phe Asn Gly Ser Val Leu Asn Glu Thr Ser Phe Ile Phe Thr	320	325	330
Glu Phe Leu Glu Pro Ala Ala Asn Glu Thr Val Arg His Gly Cys	335	340	345
Leu Arg Leu Asn Gln Pro Thr His Val Asn Asn Gly Asn Tyr Thr	350	355	360
Leu Leu Ala Ala Asn Pro Phe Gly Gln Ala Ser Ala Ser Ile Met	365	370	375
Ala Ala Phe Met Asp Asn Pro Phe Glu Phe Asn Pro Glu Asp Pro	380	385	390
Ile Pro Asp Thr Asn Ser Thr Ser Gly Asp Pro Val Glu Lys Lys	395	400	405
Asp Glu Thr Pro Phe Gly Val Ser Val Ala Val Gly Leu Ala Val	410	415	420
Phe Ala Cys Leu Phe Leu Ser Thr Leu Leu Leu Val Leu Asn Lys	425	430	435
Cys Gly Arg Arg Asn Lys Phe Gly Ile Asn Arg Pro Ala Val Leu	440	445	450
Ala Pro Glu Asp Gly Leu Ala Met Ser Leu His Phe Met Thr Leu	455	460	465
Gly Gly Ser Ser Leu Ser Pro Thr Glu Gly Lys Gly Ser Gly Leu	470	475	480
Gln Gly His Ile Ile Glu Asn Pro Gln Tyr Phe Ser Asp Ala Cys	485	490	495
Val His His Ile Lys Arg Arg Asp Ile Val Leu Lys Trp Glu Leu	500	505	510
Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys His Asn	515	520	525

Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu	
				530					535					540	
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala	
				545					550					555	
Glu	Leu	Leu	Thr	Met	Leu	Gln	His	Gln	His	Ile	Val	Arg	Phe	Phe	
				560					565					570	
Gly	Val	Cys	Thr	Glu	Gly	Arg	Pro	Leu	Leu	Met	Val	Phe	Glu	Tyr	
				575					580					585	
Met	Arg	His	Gly	Asp	Leu	Asn	Arg	Phe	Leu	Arg	Ser	His	Gly	Pro	
				590					595					600	
Asp	Ala	Lys	Leu	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Pro	Gly	Pro	
				605					610					615	
Leu	Gly	Leu	Gly	Gln	Leu	Leu	Ala	Val	Ala	Ser	Gln	Val	Ala	Ala	
				620					625					630	
Gly	Met	Val	Tyr	Leu	Ala	Gly	Leu	His	Phe	Val	His	Arg	Asp	Leu	
				635					640					645	
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Gln	Gly	Leu	Val	Val	Lys	Ile	
				650					655					660	
Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Ile	Tyr	Ser	Thr	Asp	Tyr	Tyr	
				665					670					675	
Arg	Val	Gly	Gly	Arg	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	Pro	Pro	
				680					685					690	
Glu	Ser	Ile	Leu	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val	Trp	
				695					700					705	
Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln	
				710					715					720	
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu	Ala	Ile	Asp	Cys	Ile	Thr	
				725					730					735	
Gln	Gly	Arg	Glu	Leu	Glu	Arg	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Val	
				740					745					750	
Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln	Arg	Glu	Pro	Gln	Gln	Arg	
				755					760					765	
His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg	Leu	Gln	Ala	Leu	Ala	Gln	
				770					775					780	
Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu	Gly						
				785					790						

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYYTTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGRY ARTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCCCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe
1 5 9

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp
1 5 6

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly
1 5 10 11

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	Asn	Leu	Lys
1				5					10					15
Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	Ile	Tyr	Glu
				20					25					30
Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	Arg	Ser	His
				35					40					45
Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	Pro	Gly	His
				50					55					60
Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	Val	Asn	Val
				65					70					75
Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe						
				80				84						

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